IN THE CLAIMS:

Claims 1. – 45. (cancelled)

46. (new) A forensic method of mitochondrial DNA analysis comprising the steps of:

providing a forensic evidence sample;

amplifying one or more segments of mitochondrial DNA obtained from said forensic evidence sample to obtain one or more amplification products;

determining the molecular masses of said one or more amplification products by mass spectrometry, without sequencing said one or more amplification products; and

comparing said molecular masses of said one or more amplification products with at least one database comprising a plurality of known molecular masses from said one or more segments of mitochondrial DNA from a plurality of subjects, thereby reaching a forensic conclusion.

47. (new) The forensic method of claim 46, further comprising digesting said one or more amplification products with one or more restriction enzymes to produce restriction fragments before said mass spectrometry.

48. (new) The forensic method of claim 47, wherein said one or more restriction enzymes are selected from the group consisting of *Rsa*I , *Hpa*II, *Hpy*CH4IV, *Pac*I, and *Eae*I.

49. (new) The forensic method of claim 47, further comprising determining the molecular masses of said restriction fragments by mass spectrometry, without sequencing said restriction fragments.

50. (new) The forensic method of claim 47, further comprising comparing said molecular masses of said restriction fragments with at least one database comprising a

plurality of known molecular masses from said one or more segments of mitochondrial DNA from a plurality of subjects, thereby reaching a forensic conclusion.

51. (new) The forensic method of claim 46, wherein said subjects are animals.

52. (new) The forensic method of claim 51, wherein said animals are humans.

53. (new) The forensic method of claim 46, wherein said subjects are nonhuman eukaryotic organisms, fungi, parasites or protozoa.

54. (new) The forensic method of claim 46, wherein said one or more segments of mitochondrial DNA comprises a portion of a hypervariable region of mitochondrial DNA.

55. (new) The forensic method of claim 54, wherein said hypervariable region comprises at least one of HVR1 or HVR2.

56. (new) The forensic method of claim 46, wherein said one amplification product is generated from two hypervariable portions of the noncoding region of mitochondrial DNA using flanking primers.

57. (new) The forensic method of claim 46, wherein said one or more segments of mitochondrial DNA comprises the entire mitochondrial DNA of said subject.

58. (new) The forensic method of claim 46, wherein said forensic conclusion comprises identification of at least one subject from whom said forensic evidence sample is obtained by comparing said molecular masses of said one or more amplification products with said plurality of known molecular masses in said at least one database.

59. (new) The forensic method of claim 58, wherein said forensic conclusion is the identification of a criminal.

60. (new) The forensic method of claim 58, wherein said forensic conclusion is the identification of a crime victim.

61. (new) The method of 46, further comprising determining the relative amounts of said one or more amplification products from the abundance of mass spectral peaks corresponding to said one or more amplification products.

62. (new) The forensic method of claim 46, wherein said forensic conclusion further comprises determining the movement of at least one subject from whom said forensic evidence sample is obtained by mitochondrial DNA analysis of a plurality of forensic evidence samples obtained from a plurality of locations.

63. (new) The forensic method of claim 46, wherein said mass spectrometry is electrospray Fourier transform ion cyclotron resonance mass spectrometry or electrospray time-of-flight mass spectrometry.

64. (new) The forensic method of claim 46, wherein said at least one database is a Federal Bureau of Investigation mitochondrial DNA database.

65. (new) A forensic method of mitochondrial DNA analysis comprising the steps of:

providing a forensic evidence sample;

amplifying one or more segments of mitochondrial DNA obtained from said forensic evidence sample to obtain one or more amplification products;

determining the molecular masses of said one or more amplification products by mass spectrometry, without sequencing said one or more amplification products;

calculating base compositions of said one or more amplification products from said molecular masses; and

comparing said base compositions of said one or more amplification products with at least one database comprising a plurality of known base compositions from said one or more segments of mitochondrial DNA from a plurality of subjects, thereby reaching a forensic conclusion.

66. (new) The forensic method of claim 65, further comprising digesting said one or more amplification products with one or more restriction enzymes to produce restriction fragments before said mass spectrometry.

67. (new) The forensic method of claim 66, wherein said one or more restriction enzymes are selected from the group consisting of *Rsa*I , *Hpa*II, *Hpy*CH4IV, *Pac*I, and *Eae*I.

68. (new) The forensic method of claim 66, further comprising determining the base compositions of said restriction fragments by mass spectrometry, without sequencing said restriction fragments.

69. (new) The forensic method of claim 66, further comprising comparing said base compositions of said restriction fragments with at least one database comprising a plurality of known base compositions from said one or more segments of mitochondrial DNA from a plurality of subjects, thereby reaching a forensic conclusion.

70. (new) The forensic method of claim 65, wherein said subjects are animals.

71. (new) The forensic method of claim 70, wherein said animals are humans.

72. (new) The forensic method of claim 65, wherein said subjects are nonhuman eukaryotic organisms, fungi, parasites or protozoa.

73. (new) The forensic method of claim 65, wherein said one or more segments of mitochondrial DNA comprises a portion of a hypervariable region of mitochondrial DNA.

74. (new) The forensic method of claim 73, wherein said hypervariable region comprises at least one of HVR1 or HVR2.

75. (new) The forensic method of claim 65, wherein said one amplification product is generated from two hypervariable portions of the noncoding region of mitochondrial DNA using flanking primers.

76. (new) The forensic method of claim 65, wherein said one or more segments of mitochondrial DNA comprises the entire mitochondrial DNA of said subject.

77. (new) The forensic method of claim 65, wherein said forensic conclusion comprises identification of at least one subject from whom said forensic evidence sample is obtained by comparing said molecular masses of said one or more amplification products with said plurality of known molecular masses in said at least one database.

78. (new) The forensic method of claim 77, wherein said forensic conclusion is the identification of a criminal.

79. (new) The forensic method of claim 77, wherein said forensic conclusion is the identification of a crime victim.

80. (new) The method of 65, further comprising determining the relative amounts of said one or more amplification products from the abundance of mass spectral peaks corresponding to said one or more amplification products.

81. (new) The forensic method of claim 65, wherein said forensic conclusion further comprises determining the movement of at least one subject from whom said forensic evidence sample is obtained by mitochondrial DNA analysis of a plurality of forensic evidence samples obtained from a plurality of locations.

82. (new) The forensic method of claim 65, wherein said mass spectrometry is electrospray Fourier transform ion cyclotron resonance mass spectrometry or electrospray time-of-flight mass spectrometry.

83. (new) The forensic method of claim 65, wherein said at least one database is a Federal Bureau of Investigation mitochondrial DNA database.

84. (new) A method of characterizing heteroplasmy of a segment of mitochondrial DNA of a subject comprising the steps of:

providing a sample from said subject;

amplifying said segment of mitochondrial DNA from said sample with a pair of primers to obtain a plurality of amplification products;

determining molecular masses of said plurality of amplification products by mass spectrometry, without sequencing said plurality of amplification products; and

determining base compositions of said plurality of amplification products thereby characterizing said heteroplasmy.

85. (new) The method of claim 84, wherein said heteroplasmy is selected from the group consisting of length heteroplasmy, nucleotide polymorphism heteroplasmy, or both length heteroplasmy and nucleotide polymorphism heteroplasmy.

86. (new) The method of claim 84, further comprising obtaining a plurality of samples of mitochondrial DNA from said subject at different ages of the individual, wherein the characterization of heteroplasmy indicates the rate of naturally occurring mutations in mitochondrial DNA.

87. (new) The method of claim 84, further comprising comparing said heteroplasmy in said segment of mitochondrial DNA from said sample with at least one database comprising a plurality of base compositions from said segment of mitochondrial DNA from a plurality of subjects with one or more mitochondrial diseases, wherein said comparing correlates said heteroplasmy with the onset of said one or more mitochondrial diseases in a subject.

88. (new) The method of claim 87, wherein said one or more mitochondrial diseases are selected from the group consisting of Alpers Disease, Barth syndrome, Beta-oxidation Defects, Carnitine-Acyl-Carnitine Deficiency, Carnitine Deficiency , Co-Enzyme Q10 Deficiency, Complex I Deficiency, Complex II Deficiency, Complex III Deficiency , Complex IV Deficiency, Complex V Deficiency, COX Deficiency, CPEO, CPT I Deficiency, CPT II Deficiency, Glutaric Aciduria Type II, KSS, Lactic Acidosis, LCAD, LCHAD, Leigh Disease or Syndrome, LHON, Lethal Infantile Cardiomyopathy, Luft Disease, MAD, MCA, MELAS, MERRF, Mitochondrial Cytopathy, Mitochondrial DNA Depletion, Mitochondrial Encephalopathy, Mitochondrial Myopathy, MNGIE, NARP, Pearson Syndrome, Pyruvate Carboxylase Deficiency, Pyruvate Dehydrogenase Deficiency, Respiratory Chain, SCAD, SCHAD, or VLCAD.

89. (new) The method of claim 84, wherein said mass spectrometry is electrospray Fourier transform ion cyclotron resonance mass spectrometry or electrospray time-of-flight mass spectrometry.

90. (new) The method of claim 84, wherein said sample from said subject is a forensic evidence sample.